GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 01:07:00 ; Search time 755.06 Seconds
(without alignments)
26.115 Million cell updates/sec

Title: US-09-851-670-15
Perfect score: 23
Sequence: 1 aacgtgtgcggtcctcagagaca 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101:*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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11: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
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19: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	15	65.2	38	16	AAQ99753	FBR murine sarcoma
c	2	13.6	59.1	47	21	AAZ68028	Human map-related
c	3	13.6	59.1	51	21	AAA76976	Human clone cg4291
c	4	13.4	58.3	43	22	AAC87004	Probe used to isol
	5	13.2	57.4	20	20	AAZ04950	PCR primer used to
c	6	13.2	57.4	30	20	AAX26862	PCR primer used to
c	7	13.2	57.4	42	22	AAF24109	Corynebacterium sp
c	8	13.2	57.4	54	18	AAX63345	Delta-9 desaturase
	9	13	56.5	28	21	AAA64494	Primer for triose
c	10	13	56.5	31	19	AAV67658	Nucleotide fragmen
	11	13	56.5	57	19	AAV60534	Cloned Factor X-bi
	12	12.8	55.7	24	22	AAC83968	Human 40 kDa TNF i
c	13	12.8	55.7	27	22	AAF31137	Mutagenic primer #
	14	12.8	55.7	27	22	AAF31138	Mutagenic primer #
	15	12.8	55.7	30	19	AAV45446	Human chemokine ZS
	16	12.8	55.7	47	21	AAZ67121	Human map-related
c	17	12.8	55.7	51	21	AAA76977	Human clone cg4291
c	18	12.6	54.8	21	20	AAX83520	Primer OURLess for
c	19	12.6	54.8	27	18	AAX72019	Mouse flk-1 VEGF r
c	20	12.6	54.8	31	20	AAX06550	Human biallelic po
c	21	12.6	54.8	39	22	AAH47917	Antihepatitis C PC
c	22	12.6	54.8	47	21	AAZ67626	Human map-related
c	23	12.6	54.8	47	21	AAZ69105	Human map-related
c	24	12.6	54.8	60	9	AAN81511	DNA encoding signa
	25	12.6	54.8	60	20	AAZ19576	Complement system
c	26	12.4	53.9	23	22	AAS22027	Human COL1A1 PCR p
	27	12.4	53.9	27	19	AAV37557	L. innocua 4450 sp
c	28	12.4	53.9	29	20	AAV91528	Human C-raf hammer
	29	12.4	53.9	32	19	AAV54336	T-cell receptor V-
	30	12.4	53.9	32	20	AAX55419	Primer to amplify
	31	12.4	53.9	35	15	AAQ94674	Primer, PAV, for c
c	32	12.4	53.9	36	20	AAZ08571	Anti-EGFP hammerhe
c	33	12.4	53.9	36	20	AAX78655	Anti-green fluores
c	34	12.4	53.9	37	16	AAQ83547	Elastase target mR
c	35	12.4	53.9	43	19	AAV34589	M. vaccae antigeni
c	36	12.4	53.9	43	20	AAZ11324	Mycobacterial 16S
c	37	12.4	53.9	47	21	AAZ68024	Human map-related
	38	12.4	53.9	49	22	AAF76547	Human EFEMP1 gene
	39	12.4	53.9	51	21	AAA76322	Human eph-like gen
	40	12.4	53.9	51	21	AAA76323	Human eph-like gen
c	41	12.2	53.0	19	18	AAT50892	Probe #6 for inter
	42	12.2	53.0	20	20	AAX95663	PCR primer used to
c	43	12.2	53.0	21	19	AAV31697	Exon 7 reverse pri
c	44	12.2	53.0	21	21	AAC69276	Human ABC1 gene ex
c	45	12.2	53.0	21	22	AAH62339	Transcription fact

ALIGNMENTS

RESULT 1
AAQ99753/c
ID AAQ99753 standard; RNA; 38 BP.
XX
AC AAQ99753;
XX
DT 03-MAY-1996 (first entry)
XX
DE FBR murine sarcoma virus 5'-leader region stem loop.
XX
KW FBR murine sarcoma virus; 5'-leader region stem loop;
KW Maedi-Visna virus; HIV-2; gene therapy; antisense;
KW lentiviral replication; inhibition; FBR-MuSaV; ss.
XX
OS FBR murine sarcoma virus.
XX
FH Key Location/Qualifiers
FT stem_loop 6..35
FT /*tag= a
XX
PN WO9525806-A2.
XX
PD 28-SEP-1995.
XX
PF 24-MAR-1995; 95WO-GB00663.
XX
PR 09-DEC-1994; 94GB-0025026.
PR 24-MAR-1994; 94GB-0005875.
PR 24-MAR-1994; 94GB-0005876.
XX
PA (SYNG-) SYNGENIX LTD.
XX
PI Harrison GP, Hunter E, Lever AML;
XX

```
DR   WPI; 1995-344622/44.
XX
PT   Packaging deficient lentiviruses producing lentiviral proteins -
PT   esp. for production of Maedi-Visna virus (MVV) and HIV-2 proteins,
PT   useful in gene therapy
XX
PS   Disclosure; Fig 1; 20pp; English.
XX
CC   By deleting the retroviral 5'-leader stem loop regions AAQ99744-54,
CC   in their respective viruses, a virus incapable of packaging viral
CC   RNA, but capable of producing proteins selected from the HIV-2 and
CC   Maedi-Visna virus (MVV), is produced. These viruses can be used
CC   for the integration of foreign DNA into a non-dividing cell in
CC   gene therapy, or esp. to carry DNA antisense to regions of the MMV
CC   or HIV-2 genome for the inhibition of lentiviral replication.
XX
SQ   Sequence 38 BP; 8 A; 11 C; 7 G; 12 U; 0 other;

  Query Match             65.2%;  Score 15;  DB 16;  Length 38;
  Best Local Similarity   78.3%;  Pred. No. 1.9e+02;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 aacgtgtgcggtcctcagagaca 23
          |||| ||  ||| |||||| |||
Db     27 AACGGGTCGGGTTCTCAGATACA 5


RESULT   2
AAZ68028/c
ID   AAZ68028 standard; DNA; 47 BP.
XX
AC   AAZ68028;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human map-related biallelic marker SEQ ID NO:2375.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(24,G)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;    99WO-IB00822.
XX
PR   21-APR-1998;    98US-0082614.
PR   23-NOV-1998;    98US-0109732.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome  -
XX
PS   Claim 3; Page 737; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the
CC   invention have a variety of uses: they can be used for high density
CC   mapping of the human genome, and in complex association studies and
CC   haplotyping studies which are useful in determining the genetic basis
CC   for disease states. Compositions and methods of the invention can also
CC   be useful for the identification of the targets for the development of
CC   pharmaceutical agents and diagnostic methods, as well as the
CC   characterisation of the differential efficacious responses to and side
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 47 BP; 11 A; 9 C; 15 G; 12 T; 0 other;

  Query Match             59.1%;  Score 13.6;  DB 21;  Length 47;
  Best Local Similarity   80.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      3 cgtgtgcggtcctcagagac 22
          | | ||| ||| ||||||||
Db     33 CCTTTGCAGTCATCAGAGAC 14


RESULT   3
AAA76976/c
ID   AAA76976 standard; cDNA; 51 BP.
XX
AC   AAA76976;
XX
DT   16-NOV-2000  (first entry)
XX
DE   Human clone cg42910590 polymorphic site, SEQ ID NO:659.
XX
KW   Human; single nucleotide polymorphism; SNP;
KW   detection; identification; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace (26,C)
FT                   /*tag= a
XX
PN   WO200029623-A2.
XX
PD   25-MAY-2000.
XX
PF   17-NOV-1999;    99WO-US27293.
XX
PR   17-NOV-1998;    98US-0109024.
PR   16-NOV-1999;    99US-0109024.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach MD;
XX
DR   WPI; 2000-387826/33.
XX
PT   Human nucleic acids containing single nucleotide polymorphisms, useful
PT   for treating a subject suffering, or at risk from a pathology due to
PT   the presence of a sequence polymorphism -
XX
PS   Claim 1; Page 356; 543pp; English.
XX
CC   Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC   which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC   1112 (AAA76318-A77429) are consecutive pairs of nucleotides which
CC   contain silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are
CC   consecutive pairs of nucleotides containing SNPs which result in changes
CC   in the corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC   sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
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CC   changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC   in non- conservative changes. The SNPs in sequences 1187 to 1192
CC   (AAA77504-A77509) generate frameshift mutations. The invention also
CC   relates to a method of detecting a polymorphic site in a nucleic acid and
CC   a method of determining the relatedness of two nucleic acids. It also
CC   encompasses peptides containing polymorphic sites, antibodies raised
CC   against such peptides, and a method of detecting polymorphic
CC   proteins/peptides using the antibodies. The nucleic acids are useful for
CC   gene therapy of an individual having, suspected of having, or at risk of
CC   developing a pathological condition due to the presence of a sequence
CC   polymorphism. Such treatment would comprise administration of the
CC   wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC   peptides can also be used in the treatment of such individuals.
XX
SQ   Sequence 51 BP; 12 A; 12 C; 21 G; 6 T; 0 other;


  Query Match             59.1%;  Score 13.6;  DB 21;  Length 51;
  Best Local Similarity   80.0%;  Pred. No. 1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3 cgtgtgcggtcctcagagac 22
           | |||| |||||||||  ||
Db      44 CATGTGGGGTCCTCAGCTAC 25


RESULT   4
AAC87004/c
ID   AAC87004 standard; DNA; 43 BP.
XX
AC   AAC87004;
XX
DT   20-APR-2001  (first entry)
XX
DE   Probe used to isolate cDNA encoding human polypeptide PRO4999.
XX
KW   Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW   PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW   PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW   PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW   PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW   PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
KW   probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200077037-A2.
XX
PD   21-DEC-2000.
XX
PF   22-MAY-2000; 2000WO-US14042.
XX
PR   15-JUN-1999;   99US-0139695.
PR   20-JUL-1999;   99US-0145070.
PR   26-JUL-1999;   99US-0145698.
PR   17-AUG-1999;   99US-0149396.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28301.
PR   02-DEC-1999;   99WO-US28565.
PR   07-DEC-1999;   99US-0169495.
PR   05-JAN-2000; 2000WO-US00219.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   20-MAR-2000; 2000WO-US07377.
PR   30-MAR-2000; 2000WO-US08439.
PR   15-MAY-2000; 2000WO-US13358.
PR   17-MAY-2000; 2000WO-US13705.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2001-050091/06.
XX
PT   Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT   transmembrane polypeptide is useful for gene therapy and identification
PT   of related polypeptides -
XX
PS   Example 17; Page 112; 244pp; English.
XX
CC   The present probe was used to isolate cDNA encoding a human
CC   secreted and transmembrane polypeptide. The specification describes
CC   human polypeptides, designated PRO196, PRO444, PRO183, PRO185, PRO210,
CC   PRO215, PRO217, PRO242, PRO288, PRO365, PRO1361, PRO1308, PRO1183,
CC   PRO1272, PRO1419, PRO4999, PRO7170, PRO248, PRO353, PRO1318, PRO1600,
CC   PRO9940, PRO533, PRO301, PRO187, PRO337, PRO1411, PRO4356, PRO246,
CC   PRO265, PRO941, PRO10096, PRO6003, PRO6004, PRO350, PRO2630 and PRO6309.
CC   The biological activity of cells can be modulated with agents that bind
CC   to these polypeptides, resulting in the death of the cells. The
CC   polynucleotides encoding these polypeptides are useful in the recombinant
CC   production of the polypeptides, as a hybridisation probe to screen
CC   libraries to isolate homologous sequences, or to map the gene. They may
CC   also be used for analysing genetic disorders, and to produce transgenic
CC   animals which are useful for the development and screening of
CC   therapeutically useful reagents. The polynucleotides can also be used in
CC   gene therapy e.g. to replace a defective gene.
XX
SQ   Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 other;


  Query Match             58.3%;  Score 13.4;  DB 22;  Length 43;
  Best Local Similarity   73.9%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 aacgtgtgcggtcctcagagaca 23
           ||  |||| ||| | || |||||
Db      29 AAGATGTGTGGTTCCCACAGACA 7


RESULT   5
AAZ04950
ID   AAZ04950 standard; DNA; 20 BP.
XX
AC   AAZ04950;
XX
DT   07-OCT-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW   Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW   paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW   nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer;
KW   bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS   Synthetic.
OS   Chlamydia trachomatis.
XX
PN   WO9928475-A2.
XX
PD   10-JUN-1999.
XX
PF   27-NOV-1998;   98WO-IB01939.
XX
PR   04-NOV-1998;   98US-0107077.
PR   28-NOV-1997;   97FR-0015041.
```

PR 17-DEC-1997; 97FR-0016034.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-371125/31.
XX
PT Genome sequence of Chlamydia trachomatis
XX
PS Disclosure; Page 1730; 1755pp; English.
XX
CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences
CC can also be used to control growth of the microorganism. Chlamydia
CC trachomatis is responsible for a large number of diseases, e.g. eye
CC diseases such as conventional trachoma, nonendemic trachoma,
CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC nongonococcal uretritis, epidymitis, cervicitis, salpingitis,
CC perihepatitis, bartholinitis; pneumopathy in breast feeding infants;
CC and venereal lymphogranulomatosis. The polypeptides of the
CC invention may be of use in treating these diseases.
XX
SQ Sequence 20 BP; 2 A; 2 C; 8 G; 8 T; 0 other;

Query Match 57.4%; Score 13.2; DB 20; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 cgtgtgcggtcctcagag 20
|||||| ||| || ||||
Db 1 cgtgtgtggtgcttagag 18

RESULT 6
AAX26862/c
ID AAX26862 standard; DNA; 30 BP.
XX
AC AAX26862;
XX
DT 22-JUN-1999 (first entry)
XX
DE PCR primer used to amplify murine H-Ras cDNA.
XX
KW Rin2; downregulation; functional response; allergy; asthma; hayfever;
KW Ras-dependent signalling pathway; allergy; asthma; hayfever;
KW atopic eczema; Ras-dependent cancer; neoplastic cellular proliferation;
KW autoimmune disease; T cell-associated disease;
KW T cell dependent graft vs. host disease; type I diabetes mellitus;
KW multiple sclerosis; Crohn's disease; autoimmune hepatitis; psoriasis;
KW wound healing; angiogenesis; re-epithelialization;
KW human immune deficiency virus; immune suppression; cancer therapy;
KW nerve regeneration; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9913079-A1.
XX
PD 18-MAR-1999.
XX
PF 11-SEP-1998; 98WO-US19056.
XX
PR 02-OCT-1997; 97US-0942819.
PR 11-SEP-1997; 97US-0058520.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Galli SJ, Tam S, Tsai M;
XX
DR WPI; 1999-229239/19.
XX
PT Rin2 polypeptides and related nucleic acid
XX
PS Disclosure; Page 50; 101pp; English.
XX
CC PCR primers AAX26861-62 were used to amplify murine H-Ras cDNA. The
CC specification describes Rin2 polypeptides which downregulate
CC functional responses elicited by Ras-dependent signalling pathways.
CC Agents that increase Rin2 activity (particularly Rin2 itself, optionally
CC expressed from a vector) are used to treat allergy (asthma, hayfever
CC or atopic eczema); Ras-dependent cancers and (non-)neoplastic cellular
CC proliferation; autoimmune diseases; T cell-associated diseases
CC and T cell dependent graft vs. host disease (typical examples being type
CC I diabetes mellitus; multiple sclerosis, Crohn's disease, autoimmune
CC hepatitis and psoriasis). Agents that inhibit Rin2 activity are used
CC to improve wound healing; angiogenesis and/or re-epithelialization (also
CC to improve immune response to pathogens; in human immune deficiency
CC virus, and some other, infections; immune suppression associated with
CC cancer therapy, and nerve regeneration).
XX
SQ Sequence 30 BP; 8 A; 11 C; 7 G; 4 T; 0 other;

Query Match 57.4%; Score 13.2; DB 20; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 gtgtgcggtcctcagaga 21
|||||| ||||| || ||
Db 24 GTGTGCTGTCCTGAGGGA 7

RESULT 7
AAF24109/c
ID AAF24109 standard; DNA; 42 BP.
XX
AC AAF24109;
XX
DT 22-MAR-2001 (first entry)
XX
DE Corynebacterium sp. 16S rRNA probe.
XX
KW Multi spectral identification; taxonomy; probe; 16S rRNA; ss.
XX
OS Corynebacterium sp.
XX
PN WO200075636-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US15384.
XX
PR 04-JUN-1999; 99US-0137458.
XX
PA (KAIR-) KAIROS SCI INC.
XX
PI Coleman W, Tanner M, Silva C, Bylina E, Robles M, Dilworth M;
PI Youvan D, Yang M;
XX
DR WPI; 2001-061764/07.
XX
PT Empirical calibration of optical system for multi spectral taxonomic
PT identification in biotechnology involves correcting vector data
PT representing uncorrected intensity of image pixel, by matrix
PT multiplication -
XX
PS Disclsoure; Fig 22; 93pp; English.
XX
CC The present invention relates to empirically calibrating an optical
CC system for multi spectral taxonomic identification, involving
CC collecting calibration data as spectral groups and multiplied by a
CC correction matrix. The invention is used for multi spectral taxonomic
CC identification of biological cells, particularly those of bacteria and

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CC   archaea, in complex populations of microorganisms.
XX
SQ   Sequence 42 BP; 13 A; 16 C; 6 G; 7 T; 0 other;


  Query Match             57.4%;  Score 13.2;  DB 22;  Length 42;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3 cgtgtgcggtcctcagag 20
           ||||||||  ||||  |||
Db      20 CGTGTGCGATCCTGTGAG 3


RESULT   8
AAX63345/c
ID   AAX63345 standard; RNA; 54 BP.
XX
AC   AAX63345;
XX
DT   16-JUL-1999  (first entry)
XX
DE   Delta-9 desaturase hairpin ribozyme SEQ ID NO:1220.
XX
KW   Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate;
KW   granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
KW   modulation; gene expression; transgenic plant; cleavage; canola plant;
KW   caffeine synthesis; coffee plant; nicotine production; tobacco;
KW   fruit ripening; flower pigmentation; lignin production; ss.
XX
OS   Synthetic.
OS   Zea mays.
XX
PN   WO9710328-A2.
XX
PD   20-MAR-1997.
XX
PF   12-JUL-1996;   96WO-US11689.
XX
PR   13-JUL-1995;   95US-0001135.
XX
PA   (DOWC ) DOWELANCO.
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Edington BE,  Folkerts O,  Guo L,  McSwiggen JA,  Merlo DJ;
PI   Merlo PAO,  Skokut TA,  Young SA,  Zwick MG;
XX
DR   WPI; 1997-202224/18.
XX
PT   Ribozyme which modulates plant gene expression - preferably
PT   modulates expression of DELTA-9 desaturase or granule bound starch
PT   synthase in maize or canola
XX
PS   Claim 40; Page 94; 155pp; English.
XX
CC   The present invention describes an enzymatic nucleic acid molecule (I)
CC   with RNA cleaving activity, which modulates the expression of a plant
CC   gene. Also described is a gene comprising a cDNA sequence encoding maize
CC   Delta-9 desaturase. (I) can be used to modulate expression of a gene,
CC   preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
CC   gene, in a plant (preferably a maize or canola plant). (I) can be used
CC   to modulate caffeine synthesis in a coffee plant, nicotine production in
CC   a tobacco plant, fruit ripening processes in an apple, tomato, pear,
CC   plum or peach plant, flower pigmentation in a rose, petunia,
CC   chrysanthemum or marigold plant or lignin production in a tobacco,
CC   aspen, poplar or pine plant.
XX
SQ   Sequence 54 BP; 17 A; 13 C; 12 G; 12 U; 0 other;


  Query Match             57.4%;  Score 13.2;  DB 18;  Length 54;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       6 gtgcggtcctcagagaca 23
           ||||||||  ||  |||||
Db      20 GTGCGGTCTTCTTAGACA 3


RESULT   9
AAA64494
ID   AAA64494 standard; cDNA; 28 BP.
XX
AC   AAA64494;
XX
DT   02-JAN-2001  (first entry)
XX
DE   Primer for triose phosphate isomerase gene terminator.
XX
KW   Astaxanthin synthetase; astaxanthin; beta-carotene; carotenogenic yeast;
KW   antioxidant; cancer; colouring reagent; farmed fish; salmon;
KW   triose phosphate isomerase gene; PCR primer; ss.
XX
OS   Phaffia rhodozyma.
XX
PN   EP1035206-A1.
XX
PD   13-SEP-2000.
XX
PF   03-MAR-2000; 2000EP-0104430.
XX
PR   09-MAR-1999;   99EP-0104668.
PR   01-FEB-2000; 2000EP-0101666.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Hoshino T,  Ojima K,  Setoguchi Y;
XX
DR   WPI; 2000-559874/52.
XX
PT   Novel polynucleotide encoding astaxanthin synthase useful for producing
PT   recombinant cells for producing astaxanthin from beta-carotene  -
XX
PS   Example 14; Page 16; 46pp; English.
XX
CC   PCR primers AAA64493-94 were used to amplify the triose phosphate
CC   isomerase gene terminator. The amplified sequence was used to
CC   clone DNA encoding an astaxanthin synthetase polypeptide of
CC   Phaffia rhodozyma. The enzyme is involved in the last step of the
CC   astaxanthin biosynthesis pathway, from beta-carotene to astaxanthin.
CC   P. rhodozyma is a carotenogenic yeast strain. The astaxanthin
CC   synthetase polynucleotides and polypeptides are useful for producing
CC   astaxanthin. Astaxanthin is an antioxidant which may be used to
CC   protect living cells against diseases such as cancer. Astaxanthin is
CC   also used as a colouring reagent, e.g. in farmed fish like salmon to
CC   impart an orange-red coloration.
XX
SQ   Sequence 28 BP; 6 A; 9 C; 9 G; 4 T; 0 other;


  Query Match             56.5%;  Score 13;  DB 21;  Length 28;
  Best Local Similarity   76.2%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3 cgtgtgcggtcctcagagaca 23
           ||||  ||  |||   |  ||||||
Db       7 cgtgcgcagtcgaccgagaca 27


RESULT  10
AAV67658/c
ID   AAV67658 standard; DNA; 31 BP.
XX
AC   AAV67658;
XX
DT   21-DEC-1998  (first entry)
```

```
XX
DE   Nucleotide fragment containing polymorphic site, WI-3502.
XX
KW   ss; polymorphic site; nucleic acid analysis; diagnosis; monitoring;
KW   cancer; inflammation; heart disease; CNS disease.
XX
OS   Homo sapiens.
XX
PN   WO9838846-A2.
XX
PD   11-SEP-1998.
XX
PF   06-MAR-1998;   98WO-US04571.
XX
PR   28-MAR-1997;   97US-0042125.
PR   07-MAR-1997;   97US-0813159.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Berno A,  Chee M,  Fan J,  Lipshutz RJ;
XX
DR   WPI; 1998-495419/42.
XX
PT   New nucleic acid segments containing polymorphic sites, or
PT   complements and methods of detecting a nucleic acid - for general
PT   use including diagnosis and monitoring of diseases
XX
PS   Claim 1; Page 18; 42pp; English.
XX
CC   New nucleic acid segment comprising one of the 10 - 100 bp sequences
CC   given in the specification (sequences of a polymorphic site), or the
CC   complement of the segment and a method of analysing a nucleic acid
CC   comprising determining the base occupying the polymorphic site of the
CC   polymorphic fragment sequences are disclosed in the specification.  The
CC   information obtained from nucleic acid analysis by the method described
CC   is useful in diagnosis or monitoring of diseases like cancer,
CC   inflammation, heart disease, CNS diseases, and susceptibility to
CC   infection by microorganisms. In addition, the nucleic acid segments are
CC   useful in manufacturing medication in the treatment of prophylaxis of
CC   diseases, and also the use of the DNA segments as pharmaceutical.
XX
SQ   Sequence 31 BP; 5 A; 5 C; 11 G; 9 T; 1 other;


  Query Match             56.5%;  Score 13;  DB 19;  Length 31;
  Best Local Similarity   86.7%;  Pred. No. 1.9e+03;
  Matches   13;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       9 cggtcctcagagaca 23
           | ||||||:|||||
Db      25 CTGTCCTCARAGACA 11


RESULT  11
AAV60534
ID   AAV60534 standard; DNA; 57 BP.
XX
AC   AAV60534;
XX
DT   08-DEC-1998  (first entry)
XX
DE   Cloned Factor X-binding aptamer sequence.
XX
KW   Factor X; aptamer; therapeutic; diagnosis; secondary; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "G/N"
FT   misc_feature    2
FT                   /*tag=  b
FT                   /note= "G/N"
FT   misc_feature    7
FT                   /*tag=  c
FT                   /note= "G/N"
FT   misc_feature    8
FT                   /*tag=  d
FT                   /note= "G/N"
XX
PN   US5756291-A.
XX
PD   26-MAY-1998.
XX
PF   07-JUN-1995;   95US-0484192.
XX
PR   21-AUG-1992;   92US-0934387.
PR   21-FEB-1992;   92WO-US01383.
PR   07-JUN-1995;   95US-0484192.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Albrecht G,  Griffin L,  Latham J,  Leung L,  Toole JJ;
PI   Vermaas E;
XX
DR   WPI; 1998-321524/28.
XX
PT   Assay for thrombin and purification of thrombin - using DNA aptamer
XX
PS   Example 22; Fig 6; 115pp; English.
XX
CC   AAV60515-47 represent cloned Factor X-binding aptamers. The Factor
CC   X-binding aptamers are identified using the method of the
CC   invention. The specification describes a method for identifying
CC   oligomer sequences which specifically bind target molecules such
CC   as serum proteins, kinins, eicosanoids and extracellular proteins.
CC   The method involves complexation of the target molecule with a
CC   mixture of oligonucleotides containing random sequences and sequences
CC   which serve as primer for PCR amplification. A complex is only formed
CC   with specifically binding oligonucleotide sequences. The complex is
CC   isolated, and complexed members of the oligonucleotide mixture are
CC   recovered by PCR. The method can be used to generate aptamers that can
CC   be used for therapeutic and diagnostic purposes, and for generating
CC   secondary aptamers.
XX
SQ   Sequence 57 BP; 10 A; 10 C; 22 G; 9 T; 6 other;


  Query Match             56.5%;  Score 13;  DB 19;  Length 57;
  Best Local Similarity   76.2%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3 cgtgtgcggtcctcagagaca 23
           ||  ||||||| ||| ||| |
Db       9 cggatgcggtcgtcacagaga 29


RESULT  12
AAC83968
ID   AAC83968 standard; DNA; 24 BP.
XX
AC   AAC83968;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human 40 kDa TNF inhibitor probe #7.
XX
KW   TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
KW   IL-1; inflammatory disease; degenerative disease; human; probe;
KW   lymphotoxin; ss.
XX
OS   Homo sapiens.
XX
PN   US6143866-A.
XX
```

PD 07-NOV-2000.
XX
PF 19-JAN-1995; 95US-0375242.
XX
PR 19-JUL-1990; 90US-0555274.
PR 09-JUL-1993; 93US-0090366.
PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.
PR 07-FEB-1990; 90US-0479661.
XX
PA (AMGE-) AMGEN INC.
XX
PI Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
PI Vanderslice RW, Vannice J, Kohno T;
XX
DR WPI; 2001-006443/01.
XX
PT Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT non-native cysteine residue cross-linked with polyethylene glycol,
PT useful for treating inflammatory and degenerative diseases mediated by
PT TNF -
XX
PS Example 14; Column 35; 82pp; English.
XX
CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC novel TNF inhibitors of the present invention are useful as therapeutic
CC agents for inhibiting the activity of TNF and interleukin (IL-1), and
CC for treating inflammatory and degenerative diseases mediated by TNF. The
CC present sequence is a probe for the coding sequence for 40 kDa TNF
CC inhibitor (AAC83951 and AAB37685). The 40 kDa TNF inhibitor can inhibit
CC both TNF alpha and beta (lymphotoxin).
XX
SQ Sequence 24 BP; 3 A; 6 C; 9 G; 6 T; 0 other;

Query Match 55.7%; Score 12.8; DB 22; Length 24;
Best Local Similarity 87.5%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 tgtgcggtcctcagag 20
|||||| ||||||| ||
Db 8 tgtgctgtcctcacag 23

RESULT 13
AAF31137/c
ID AAF31137 standard; DNA; 27 BP.
XX
AC AAF31137;
XX
DT 27-APR-2001 (first entry)
XX
DE Mutagenic primer #16 for human SAH.
XX
KW Analyte-binding enzyme; analyte analysis; mutagenic primer; ss.
XX
OS Homo sapiens.
XX
PN WO200102600-A2.
XX
PD 11-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US18057.
XX
PR 06-JUL-1999; 99US-0347878.
PR 06-DEC-1999; 99US-0457205.
XX
PA (GEAT) GEN ATOMICS.
XX
PI Yuan C;
XX
DR WPI; 2001-071583/08.
XX
PT Assaying method, useful for prognosis and diagnosis of disease,
PT comprises contacting sample with a mutant analyte-binding enzyme and
PT detecting binding -
XX
PS Example 1; Page 152; 187pp; English.
XX
CC The present invention relates to a method for assaying an analyte in a
CC sample comprising: contacting the sample with a mutant analyte-binding
CC enzyme which has binding affinity for the analyte or an immediate
CC analyte enzymatic conversion product but has attenuated catalytic
CC activity; and detecting resulting binding. The method is useful in
CC monitoring biological systems/processes, or prognosis/diagnosis of
CC disease caused by imbalances of the analytes. The present sequence is
CC a mutagenic primer used in the present invention.
XX
SQ Sequence 27 BP; 6 A; 8 C; 9 G; 4 T; 0 other;

Query Match 55.7%; Score 12.8; DB 22; Length 27;
Best Local Similarity 87.5%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 gtgcggtcctcagaga 21
||| ||||||||||
Db 20 GTGGTGTCCTCAGAGA 5

RESULT 14
AAF31138
ID AAF31138 standard; DNA; 27 BP.
XX
AC AAF31138;
XX
DT 27-APR-2001 (first entry)
XX
DE Mutagenic primer #17 for human SAH.
XX
KW Analyte-binding enzyme; analyte analysis; mutagenic primer; ss.
XX
OS Homo sapiens.
XX
PN WO200102600-A2.
XX
PD 11-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US18057.
XX
PR 06-JUL-1999; 99US-0347878.
PR 06-DEC-1999; 99US-0457205.
XX
PA (GEAT) GEN ATOMICS.
XX
PI Yuan C;
XX
DR WPI; 2001-071583/08.
XX
PT Assaying method, useful for prognosis and diagnosis of disease,
PT comprises contacting sample with a mutant analyte-binding enzyme and
PT detecting binding -
XX
PS Example 1; Page 152; 187pp; English.
XX
CC The present invention relates to a method for assaying an analyte in a
CC sample comprising: contacting the sample with a mutant analyte-binding
CC enzyme which has binding affinity for the analyte or an immediate
CC analyte enzymatic conversion product but has attenuated catalytic
CC activity; and detecting resulting binding. The method is useful in
CC monitoring biological systems/processes, or prognosis/diagnosis of
CC disease caused by imbalances of the analytes. The present sequence is
CC a mutagenic primer used in the present invention.
XX
SQ Sequence 27 BP; 4 A; 9 C; 8 G; 6 T; 0 other;

Query Match 55.7%; Score 12.8; DB 22; Length 27;
Best Local Similarity 87.5%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       6 gtgcggtcctcagaga 21
           |||  ||||||||||
Db       8 gtggtgtcctcagaga 23
```

RESULT 15
AAV45446
ID AAV45446 standard; cDNA; 30 BP.
XX
AC AAV45446;
XX
DT 02-FEB-1999 (first entry)
XX
DE Human chemokine ZSIG-35 DNA probe ZC12449.
XX
KW ZSIG-35; beta-chemokine; human; ligand; lymphocyte migration;
KW inflammation; ischaemia; reperfusion injury; probe; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9844117-A1.
XX
PD 08-OCT-1998.
XX
PF 27-MAR-1998; 98WO-US06115.
XX
PR 09-MAY-1997; 97US-0046083.
PR 28-MAR-1997; 97US-0042862.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sheppard PO;
XX
DR WPI; 1998-557114/47.
XX
PT New human chemokine ZSIG-35 - used for, e.g. treating inflammatory
PT disease, lymphocyte migration and ischaemia/reperfusion injury
XX
PS Example 2; Page 85; 105pp; English.
XX
CC Probe ZC12449 has been radiolabelled at the 5' end and used in
CC Northern blots to determine the tissue distribution of novel human
CC beta-chemokine ZSIG-35 expression. A 1 kb transcript was detected
CC in thymus and small intestine. ZSIG-35 polypeptides of the
CC invention can be used in therapeutics for the regulation of acute
CC and chronic inflammatory disease conditions, lymphocyte migration
CC and ischaemia/reperfusion injury.
XX
SQ Sequence 30 BP; 9 A; 8 C; 9 G; 4 T; 0 other;

Query Match 55.7%; Score 12.8; DB 19; Length 30;
Best Local Similarity 87.5%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       8 gcggtcctcagagaca 23
           || ||||||| |||||
Db      15 gcagtcctcaaagaca 30
```

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